

#2  
OIPE

## RAW SEQUENCE LISTING

DATE: 07/24/2001

PATENT APPLICATION: US/09/904,954

TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

## SEQUENCE LISTING

4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: BECKMANN, M. P.  
7 CERRETTI, DOUGLAS P.  
9 (ii) TITLE OF INVENTION: CYTOKINE THAT BINDS THE CELL SURFACE  
10 RECEPTOR HEK  
12 (iii) NUMBER OF SEQUENCES: 4  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: IMMUNEX CORPORATION  
16 (B) STREET: 51 UNIVERSITY STREET  
17 (C) CITY: SEATTLE  
18 (D) STATE: WASHINGTON  
19 (E) COUNTRY: USA  
20 (F) ZIP: 98101  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Floppy disk  
24 (B) COMPUTER: Apple Macintosh  
25 (C) OPERATING SYSTEM: Apple System 7.1  
26 (D) SOFTWARE: Microsoft Word for Apple, Version 5.1a  
28 (vi) CURRENT APPLICATION DATA:  
C--> 29 (A) APPLICATION NUMBER: US/09/904,954  
C--> 30 (B) FILING DATE: 12-Jul-2001  
31 (C) CLASSIFICATION:  
41 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 08/240,124  
35 (B) FILING DATE:  
38 (A) APPLICATION NUMBER: US 08/114,426  
39 (B) FILING DATE: 30-AUG-1993  
42 (A) APPLICATION NUMBER: US 08/109,745  
43 (B) FILING DATE: 20-AUG-1993  
45 (viii) ATTORNEY/AGENT INFORMATION:  
46 (A) NAME: SEESE, KATHRYN A.  
47 (B) REGISTRATION NUMBER: 32,172  
48 (C) REFERENCE/DOCKET NUMBER: 2814-C  
50 (ix) TELECOMMUNICATION INFORMATION:  
51 (A) TELEPHONE: (206) 587-0430  
52 (B) TELEFAX: (206) 233-0644  
53 (C) TELEX: 756822  
56 (2) INFORMATION FOR SEQ ID NO: 1:  
58 (i) SEQUENCE CHARACTERISTICS:  
59 (A) LENGTH: 1037 base pairs  
60 (B) TYPE: nucleic acid  
61 (C) STRANDEDNESS: single  
62 (D) TOPOLOGY: linear  
64 (ii) MOLECULE TYPE: cDNA to mRNA  
66 (iii) HYPOTHETICAL: NO  
68 (iv) ANTI-SENSE: NO

ENTERED

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001

TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

```

71 (vii) IMMEDIATE SOURCE:
72 (B) CLONE: hek-L A2
74 (ix) FEATURE:
75 (A) NAME/KEY: CDS
76 (B) LOCATION: 83..799
78 (ix) FEATURE:
79 (A) NAME/KEY: sig_peptide
80 (B) LOCATION: 83..139
82 (ix) FEATURE:
83 (A) NAME/KEY: mat_peptide
84 (B) LOCATION: 140..796
87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
89 GGATCTTGGA ACGAGACGAC CTGCTGGAGA AGCCGGGAGC GCGGGGCTCA GTCGGGGGGC 60
91 GCGGGCGGCG GCGGCTCCGG GG ATG GCG GCG GCT CCG CTG CTG CTG CTG CTG 112
92 Met Ala Ala Ala Pro Leu Leu Leu Leu Leu
93 -19 -15 -10
95 CTG CTC GTG CCC GTG CCG CTG CTG CCG CTG CTG GCC CAA GGG CCC GGA 160
96 Leu Leu Val Pro Val Pro Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly
97 -5 1 5
99 GGG GCG CTG GGA AAC CGG CAT GCG GTG TAC TGG AAC AGC TCC AAC CAG 208
100 Gly Ala Leu Gly Asn Arg His Ala Val Tyr Trp Asn Ser Ser Asn Gln
101 10 15 20
103 CAC CTG CGG CGA GAG GGC TAC ACC GTG CAG GTG AAC GTG AAC GAC TAT 256
104 His Leu Arg Arg Glu Gly Tyr Thr Val Gln Val Asn Val Asn Asp Tyr
105 25 30 35
107 CTG GAT ATT TAC TGC CCG CAC TAC AAC AGC TCG GGG GTG GGC CCC GGG 304
108 Leu Asp Ile Tyr Cys Pro His Tyr Asn Ser Ser Gly Val Gly Pro Gly
109 40 45 50 55
111 GCG GGA CCG GGG CCC GGA GGC GGG GCA GAG CAG TAC GTG CTG TAC ATG 352
112 Ala Gly Pro Gly Pro Gly Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met
113 60 65 70
115 GTG AGC CGC AAC GGC TAC CGC ACC TGC AAC GCC AGC CAG GGC TTC AAG 400
116 Val Ser Arg Asn Gly Tyr Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys
117 75 80 85
119 CGC TGG GAG TGC AAC CGG CCG CAC GCC CCG CAC AGC CCC ATC AAG TTC 448
120 Arg Trp Glu Cys Asn Arg Pro His Ala Pro His Ser Pro Ile Lys Phe
121 90 95 100
123 TCG GAG AAG TTC CAG CGC TAC AGC GCC TTC TCT CTG GGC TAC GAG TTC 496
124 Ser Glu Lys Phe Gln Arg Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe
125 105 110 115
127 CAC GCC GGC CAC GAG TAC TAC TAC ATC TCC ACG CCC ACT CAC AAC CTG 544
128 His Ala Gly His Glu Tyr Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu
129 120 125 130 135
131 CAC TGG AAG TGT CTG AGG ATG AAG GTG TTC GTC TGC TGC GCC TCC ACA 592
132 His Trp Lys Cys Leu Arg Met Lys Val Phe Val Cys Cys Ala Ser Thr
133 140 145 150
135 TCG CAC TCC GGG GAG AAG CCG GTC CCC ACT CTC CCC CAG TTC ACC ATG 640
136 Ser His Ser Gly Glu Lys Pro Val Pro Thr Leu Pro Gln Phe Thr Met
137 155 160 165

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001

TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

139 GGC CCC AAT GTG AAG ATC AAC GTG CTG GAA GAC TTT GAG GGA GAG AAC 688  
 140 Gly Pro Asn Val Lys Ile Asn Val Leu Glu Asp Phe Glu Gly Glu Asn  
 141 170 175 180  
 143 CCT CAG GTG CCC AAG CTT GAG AAG AGC ATC AGC GGG ACC AGC CCC AAA 736  
 144 Pro Gln Val Pro Lys Leu Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys  
 145 185 190 195  
 147 CGG GAA CAC CTG CCC CTG GCC GTG GGC ATC GCC TTC TTC CTC ATG ACG 784  
 148 Arg Glu His Leu Pro Leu Ala Val Gly Ile Ala Phe Phe Leu Met Thr  
 149 200 205 210 215  
 151 TTC TTG GCC TCC TAGCTCTGCC CCCTCCCCTG GGGGGGGAGA GATGGGGCGG 836  
 152 Phe Leu Ala Ser  
 W--> 153 220  
 155 GGCTTGGAAG GAGCAGGGAG CCTTTGGCCT CTCCAAGGGA AGCCTAGTGG GCCTAGACCC 896  
 157 CTCCTCCCAT GGCTAGAAGT GGGGCCTGCA CCATACATCT GTGTCCGCCC CCTCTACCCC 956  
 159 TTCCCCCACC GTAGGGCACT GTAGTGGACC AAGCACGGGG ACAGCCATGG GTCCCAGCA 1016  
 161 GGTCGTCTCG TTCCAAGATC C 1037  
 164 (2) INFORMATION FOR SEQ ID NO: 2:  
 166 (i) SEQUENCE CHARACTERISTICS:  
 167 (A) LENGTH: 238 amino acids  
 168 (B) TYPE: amino acid  
 169 (D) TOPOLOGY: linear  
 171 (ii) MOLECULE TYPE: protein  
 173 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 175 Met Ala Ala Ala Pro Leu Leu Leu Leu Leu Leu Val Pro Val Pro  
 176 -19 -15 -10 -5  
 178 Leu Leu Pro Leu Leu Ala Gln Gly Pro Gly Gly Ala Leu Gly Asn Arg  
 179 1 5 10  
 181 His Ala Val Tyr Trp Asn Ser Ser Asn Gln His Leu Arg Arg Glu Gly  
 182 15 20 25  
 184 Tyr Thr Val Gln Val Asn Val Asn Asp Tyr Leu Asp Ile Tyr Cys Pro  
 185 30 35 40 45  
 187 His Tyr Asn Ser Ser Gly Val Gly Pro Gly Ala Gly Pro Gly Pro Gly  
 188 50 55 60  
 190 Gly Gly Ala Glu Gln Tyr Val Leu Tyr Met Val Ser Arg Asn Gly Tyr  
 191 65 70 75  
 193 Arg Thr Cys Asn Ala Ser Gln Gly Phe Lys Arg Trp Glu Cys Asn Arg  
 194 80 85 90  
 196 Pro His Ala Pro His Ser Pro Ile Lys Phe Ser Glu Lys Phe Gln Arg  
 197 95 100 105  
 199 Tyr Ser Ala Phe Ser Leu Gly Tyr Glu Phe His Ala Gly His Glu Tyr  
 200 110 115 120 125  
 202 Tyr Tyr Ile Ser Thr Pro Thr His Asn Leu His Trp Lys Cys Leu Arg  
 203 130 135 140  
 205 Met Lys Val Phe Val Cys Cys Ala Ser Thr Ser His Ser Gly Glu Lys  
 206 145 150 155  
 208 Pro Val Pro Thr Leu Pro Gln Phe Thr Met Gly Pro Asn Val Lys Ile  
 209 160 165 170  
 211 Asn Val Leu Glu Asp Phe Glu Gly Glu Asn Pro Gln Val Pro Lys Leu  
 212 175 180 185

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001

TIME: 11:32:58

Input Set : N:\Crf3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

```

214 Glu Lys Ser Ile Ser Gly Thr Ser Pro Lys Arg Glu His Leu Pro Leu
215 190                      195                      200                      205
217 Ala Val Gly Ile Ala Phe Phe Leu Met Thr Phe Leu Ala Ser
218                      210                      215
221 (2) INFORMATION FOR SEQ ID NO: 3:
223     (i) SEQUENCE CHARACTERISTICS:
224         (A) LENGTH: 636 base pairs
225         (B) TYPE: nucleic acid
226         (C) STRANDEDNESS: single
227         (D) TOPOLOGY: linear
229     (ii) MOLECULE TYPE: cDNA to mRNA
231     (iii) HYPOTHETICAL: NO
233     (iv) ANTI-SENSE: NO
236     (vii) IMMEDIATE SOURCE:
237         (B) CLONE: hek-L C6
239     (ix) FEATURE:
240         (A) NAME/KEY: mat_peptide
241         (B) LOCATION: 94..630
243     (ix) FEATURE:
244         (A) NAME/KEY: CDS
245         (B) LOCATION: 28..633
247     (ix) FEATURE:
248         (A) NAME/KEY: sig_peptide
249         (B) LOCATION: 28..93
252     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
254 GCCAGACCAA ACCGGACCTC GGGGGCG ATG CGG CTG CTG CCC CTG CTG CGG      51
255                               Met Arg Leu Leu Pro Leu Leu Arg
256                               -22   -20                       -15
258 ACT GTC CTC TGG GCC GCG TTC CTC GGC TCC CCT CTG CGC GGC GGC TCC      99
259 Thr Val Leu Trp Ala Ala Phe Leu Gly Ser Pro Leu Arg Gly Gly Ser
260                               -10                       -5                       1
262 AGC CTC CGC CAC GTA GTC TAC TGG AAC TCC AGT AAC CCC AGG TTG CTT      147
263 Ser Leu Arg His Val Val Tyr Trp Asn Ser Ser Asn Pro Arg Leu Leu
264                               5                       10                       15
266 CGA GGA GAC GCC GTG GTG GAG CTG GGC CTC AAC GAT TAC CTA GAC ATT      195
267 Arg Gly Asp Ala Val Val Glu Leu Gly Leu Asn Asp Tyr Leu Asp Ile
268       20                      25                      30
270 GTC TGC CCC CAC TAC GAA GGC CCA GGG CCC CCT GAG GGC CCC GAG ACG      243
271 Val Cys Pro His Tyr Glu Gly Pro Gly Pro Pro Glu Gly Pro Glu Thr
272  35                      40                      45                      50
274 TTT GCT TTG TAC ATG GTG GAC TGG CCA GGC TAT GAG TCC TGC CAG GCA      291
275 Phe Ala Leu Tyr Met Val Asp Trp Pro Gly Tyr Glu Ser Cys Gln Ala
276                      55                      60                      65
278 GAG GGC CCC CGG GCC TAC AAG CGC TGG GTG TGC TCC CTG CCC TTT GGC      339
279 Glu Gly Pro Arg Ala Tyr Lys Arg Trp Val Cys Ser Leu Pro Phe Gly
280                      70                      75                      80
282 CAT GTT CAA TTC TCA GAG AAG ATT CAG CGC TTC ACA CCT TTC TCC CTC      387
283 His Val Gln Phe Ser Glu Lys Ile Gln Arg Phe Thr Pro Phe Ser Leu
284                      85                      90                      95

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001

TIME: 11:32:58

Input Set : N:\Crif3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

```

286 GGC TTT GAG TTC TTA CCT GGA GAG ACT TAC TAC TAC ATC TCG GTG CCC      435
287 Gly Phe Glu Phe Leu Pro Gly Glu Thr Tyr Tyr Tyr Ile Ser Val Pro
288   100                               105                               110
290 ACT CCA GAG AGT TCT GGC CAG TGC TTG AGG CTC CAG GTG TCT GTC TGC      483
291 Thr Pro Glu Ser Ser Gly Gln Cys Leu Arg Leu Gln Val Ser Val Cys
292 115                               120                               125                               130
294 TGC AAG GAG AGG AAG TCT GAG TCA GCC CAT CCT GTT GGG AGC CCT GGA      531
295 Cys Lys Glu Arg Lys Ser Glu Ser Ala His Pro Val Gly Ser Pro Gly
296                               135                               140                               145
298 GAG AGT GGC ACA TCA GGG TGG CGA GGG GGG GAC ACT CCC AGC CCC CTC      579
299 Glu Ser Gly Thr Ser Gly Trp Arg Gly Gly Asp Thr Pro Ser Pro Leu
300                               150                               155                               160
302 TGT CTC TTG CTA TTA CTG CTG CTT CTG ATT CTT CGT CTT CTG CGA ATT      627
303 Cys Leu Leu Leu Leu Leu Leu Leu Leu Ile Leu Arg Leu Leu Arg Ile
304                               165                               170                               175
306 CTG TGAGCC
307 Leu

```

W--&gt; 308 180

312 (2) INFORMATION FOR SEQ ID NO: 4:

314 (i) SEQUENCE CHARACTERISTICS:

315 (A) LENGTH: 201 amino acids

316 (B) TYPE: amino acid

317 (D) TOPOLOGY: linear

319 (ii) MOLECULE TYPE: protein

321 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```

323 Met Arg Leu Leu Pro Leu Leu Arg Thr Val Leu Trp Ala Ala Phe Leu
324 -22 -20 -15 -10
326 Gly Ser Pro Leu Arg Gly Gly Ser Ser Leu Arg His Val Val Tyr Trp
327 -5 1 5 10
329 Asn Ser Ser Asn Pro Arg Leu Leu Arg Gly Asp Ala Val Val Glu Leu
330 15 20 25
332 Gly Leu Asn Asp Tyr Leu Asp Ile Val Cys Pro His Tyr Glu Gly Pro
333 30 35 40
335 Gly Pro Pro Glu Gly Pro Glu Thr Phe Ala Leu Tyr Met Val Asp Trp
336 45 50 55
338 Pro Gly Tyr Glu Ser Cys Gln Ala Glu Gly Pro Arg Ala Tyr Lys Arg
339 60 65 70
341 Trp Val Cys Ser Leu Pro Phe Gly His Val Gln Phe Ser Glu Lys Ile
342 75 80 85 90
344 Gln Arg Phe Thr Pro Phe Ser Leu Gly Phe Glu Phe Leu Pro Gly Glu
345 95 100 105
347 Thr Tyr Tyr Tyr Ile Ser Val Pro Thr Pro Glu Ser Ser Gly Gln Cys
348 110 115 120
350 Leu Arg Leu Gln Val Ser Val Cys Cys Lys Glu Arg Lys Ser Glu Ser
351 125 130 135
353 Ala His Pro Val Gly Ser Pro Gly Glu Ser Gly Thr Ser Gly Trp Arg
354 140 145 150
356 Gly Gly Asp Thr Pro Ser Pro Leu Cys Leu Leu Leu Leu Leu
357 155 160 165 170

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/904,954

DATE: 07/24/2001

TIME: 11:32:59

Input Set : N:\Crif3\RULE60\09904954.txt

Output Set: N:\CRF3\07242001\I904954.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:153 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

L:308 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3